AMENDMENTS TO THE CLAIMS

1. – 19. (Canceled)

20. (New) A glutamic acid synthesizing gene selected from the group consisting of glutamate dehydrogenase, citrate synthase, isocitrate synthase, pyruvate dehydrogenase, and aconitase, comprising a DNA sequence situated at position -35 in a promoter sequence of the glutamic acid synthesizing gene, wherein said DNA sequence is selected from the group consisting of CGGTCA, TTGTCA, TTGACA, and TTGCCA.

21. (New) The glutamic acid synthesizing gene of Claim 20, which is glutamate dehydrogenase.

22. (New) The glutamic acid synthesizing gene of Claim 20, which is citrate synthase.

23. (New) The glutamic acid synthesizing gene of Claim 20, which is isocitrate synthase.

24. (New) The glutamic acid synthesizing gene of Claim 20, which is pyruvate dehydrogenase.

25. (New) The glutamic acid synthesizing gene of Claim 20, which is aconitase.

26. (New) The glutamic acid synthesizing gene of Claim 20, further comprising TATAAT or CATAAT situated at position -10 in the promoter sequence.

27. (New) The glutamic acid synthesizing gene of Claim 20, wherein said DNA sequence is CGGTCA.

28. (New) The glutamic acid synthesizing gene of Claim 20, wherein said DNA sequence is TTGTCA.

29. (New) The glutamic acid synthesizing gene of Claim 20, wherein said DNA sequence is TTGACA.

30. (New) The glutamic acid synthesizing gene of Claim 20, wherein said DNA sequence is TTGCCA.

31. (New) The glutamic acid synthesizing gene of Claim 20, which is citrate synthase and wherein said DNA sequence is TTGACA.

32. (New) The glutamic acid synthesizing gene of Claim 31, further comprising TATAAT situated at position -10 in the promoter sequence.

33. (New) The glutamic acid synthesizing gene of Claim 20, which is isocitrate synthase and wherein said DNA sequence is TTGCCA or TTGACA.

34. (New) The glutamic acid synthesizing gene of Claim 33, further comprising TATAAT situated at position -10 in the promoter sequence.

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35. (New) The glutamic acid synthesizing gene of Claim 20, which is pyruvate dehydrogenase and wherein said DNA sequence is TTGCCA.

36. (New) The glutamic acid synthesizing gene of Claim 35, further comprising TATAAT.

37. (New) A coryneform bacterium comprising the glutamic acid synthesizing gene of Claim 20.